

6455266

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SEQ ID NO. 1

10	20	30	40
GACCAATCGGAGTGTGGTGAATTTTTGGAAAATATTTTGTGCGGTTCC			
50	60	70	80
TTTAGTTGTGTAATATAGTACTTTAGTTACAAATTTGGAATAATTTGG			
100	110	120	130
CAGCAAAACCATCTGCAGCAACAAATCATCTGCAGCTGCGAAATCAT			
150	160	170	180
CTGCAGCAGCAAAAGCATCTTCAGGAGCGAGAAAAGCCCCAAATAATG			
200	210	220	
TGAG ATG GCA GTT GAC GTC CGA ATC GCT GCC TTC			
Met Ala Val Asp Val Arg Ile Ala Ala Phe			
230	240	250	260
CTG CTG GTG TTT ATA GCG CCT GCA GTT TTA GCT CAA			
Leu Leu Val Phe Ile Ala Pro Ala Val Leu Ala Gln			
270	280	290	
GAG AGA TGT GGG TAT ATG ACC GCC ATC CCA AGG CTA			
Glu Arg Cys Gly Tyr Met Thr Ala Ile Pro Arg Leu			
300	310	320	330
CCA CGA CCG GAT AAT TTG CCA GTA CTA AAT TTT GAA			
Pro Arg Pro Asp Asn Leu Pro Val Leu Asn Phe Glu			
340	350	360	370
GGC CAG ACA TGG AGT CAG AGG CCC CTG CTC CCC GCC			
Gly Gln Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala			
380	390	400	
CCG GAG CGG GAT GAC CTG TGC ATG GAC GCC TAC CAC			
Pro Glu Arg Asp Asp Leu Cys Met Asp Ala Tyr His			
410	420	430	440
GTG ATA ACA GCC AAC CTC GGC ACG CAG GTC ATC TAC			
Val Ile Thr Ala Asn Leu Gly Thr Gln Val Ile Tyr			
450	460	470	
ATG GAT GAA GAG ATA GAA GAC GAA ATC ACC ATC GCC			
Met Asp Glu Glu Ile Glu Asp Glu Ile Thr Ile Ala			
480	490	500	510
ATA CTT AAT TAT AAC GGA CCA TCA ACT CCG TTC ATT			
Ile Leu Asn Tyr Asn Gly Pro Ser Thr Pro Phe Ile			

FIG. 1A

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520 530 540 550
 GAA CTG CCA TTT TTA TCC GGT TCG TAC AAT CTG CTG
 Glu Leu Pro Phe Leu Ser Gly Ser Tyr Asn Leu Leu
 560 570 580
 ATG CCG GTC ATC AGG AGA GTT GAC AAC GGG GAG TGG
 Met Pro Val Ile Arg Arg Val Asp Asn Gly Glu Trp
 590 600 610 620
 CAT CTC ATC ATC ACG CAA AGA CAG CAT TAC GAG TTG
 His Leu Ile Ile Thr Gln Arg Gln His Tyr Glu Leu
 630 640 650
 CCC GGC ATG CAG CAG TAC ATG TTC AAT GTG CGC GTG
 Pro Gly Met Gln Gln Tyr Met Phe Asn Val Arg Val
 660 670 680 690
 GAC GGC CAG TCG CTG GTG GCA GGC GTG TCT CTC GCT
 Asp Gly Gln Ser Leu Val Ala Gly Val Ser Leu Ala
 700 710 720 730
 ATC GTC AAC ATA GAT GAC AAC GCG CCC ATC ATA CAA
 Ile Val Asn Ile Asp Asp Asn Ala Pro Ile Ile Gln
 740 750 760
 AAC TTC GAG CCT TGC CGG GTT CCT GAA CTG GGC GAG
 Asn Phe Glu Pro Cys Arg Val Pro Glu Leu Gly Glu
 770 780 790 800
 CCA GGG TTG ACA GAA TGC ACA TAC CAA GTA TCG GAC
 Pro Gly Leu Thr Glu Cys Thr Tyr Gln Val Ser Asp
 810 820 830
 GCG GAC GGA CGG ATC AGC ACA GAG TTC ATG ACG TTC
 Ala Asp Gly Arg Ile Ser Thr Glu Phe Met Thr Phe
 840 850 860 870
 AGG ATC GAC AGC GTT CGT GGC GAC GAG GAG ACC TTC
 Arg Ile Asp Ser Val Arg Gly Asp Glu Glu Thr Phe
 880 890 900 910
 TAC ATC GAA CGG ACG AAT ATC CCC AAC CAA TGG ATG
 Tyr Ile Glu Arg Thr Asn Ile Pro Asn Gln Trp Met
 920 930 940
 TGG CTA AAT ATG ACC ATA GGC GTT AAT ACC TCG CTC
 Trp Leu Asn Met Thr Ile Gly Val Asn Thr Ser Leu

FIG. 1B

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950 AAC TTC GTC ACC AGT CCG CTG CAT ATA TTC AGC GTG
 Asn Phe Val Thr Ser Pro Leu His Ile Phe Ser Val
 960 970 980
 990 1000 1010
 ACA GCC CTG GAC TCG CTC CCG AAC ACC CAC ACG GTG
 Thr Ala Leu Asp Ser Leu Pro Asn Thr His Thr Val
 1020 1030 1040 1050
 ACT ATG ATG GTG CAA GTG GCG AAT GTG AAC AGC
 Thr Met Met Val Gln Val Ala Asn Val Asn Ser
 1060 1070 1080
 CGT CCG CCG CGC TGG CTG GAG ATC TTC GCT GTC CAA
 Arg Pro Pro Arg Trp Leu Glu Ile Phe Ala Val Gln
 1090 1100 1110 1120
 CAG TTT GAA GAG AAA TCT TAC CAA AAC TTC ACA
 Gln Phe Glu Glu Lys Ser Tyr Gln Asn Phe Thr
 1130 1140 1150
 GTG AGG GCG ATC GAC GGA GAC ACT GAG ATC AAT ATG
 Val Arg Ala Ile Asp Gly Asp Thr Glu Ile Asn Met
 1160 1170 1180 1190
 CCT ATC AAC TAC AGG CTG ATC ACA AAT GAG GAA GAC
 Pro Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp
 1200 1210 1220
 ACA TTC TTC AGC ATT GAG GCC CTG CCT GGT GGA AAA
 Thr Phe Phe Ser Ile Glu Ala Leu Pro Gly Gly Lys
 1230 1240 1250 1260
 AGC GGG GCT GTA TTC CTC GTG TCG CCA ATT GAC
 Ser Gly Ala Val Phe Leu Val Ser Pro Ile Asp
 1270 1280 1290
 CGC GAC ACA CTG CAA CGA GAG GTG TTT CCA CTT ACG
 Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr
 1300 1310 1320 1330
 ATC GTC GCT TAC AAA TAT GAT GAG GAG GCC TTC TCC
 Ile Val Ala Tyr Lys Tyr Asp Glu Glu Ala Phe Ser
 1340 1350 1360
 ACA TCA ACA AAC GTG GTC ATC ATT GTG ACA GAC ATC
 Thr Ser Thr Asn Val Val Ile Ile Val Thr Asp Ile

FIG. 1C

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1370 1380 1390 1400
 AAC GAC CAA AGA CCT GAA CCT ATA CAC AAG GAA
 Asn Asp Gln Arg Pro Glu Pro Ile His Lys Glu
 1410 1420 1430
 TAT CGA CTG GCA ATC ATG GAG GAG ACG CCC CTG ACC
 Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr
 1440 1450 1460 1470
 CTC AAC TTC GAT AAA GAA TTC GGA TTT CAT GAT
 Leu Asn Phe Asp Lys Glu Phe Gly Phe His Asp
 1480 1490 1500
 AAG GAT TTA GGT CAA AAC GCT CAG TAC ACG GTG CGT
 Lys Asp Leu Gly Gln Asn Ala Gln Tyr Thr Val Arg
 1510 1520 1530 1540
 CTA GAG AGC GTG GAC CCT CCA GGC GCT GCT GAG GCA
 Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala
 1550 1560 1570
 TTC TAC ATA GCG CCT GAA GTC GGC TAC CAG CGA CAG
 Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln
 1580 1590 1600 1610
 ACC TTC ATC ATG GGC ACC CTC AAT CAC TCC ATG
 Thr Phe Ile Met Gly Thr Leu Asn His Ser Met
 1620 1630 1640
 CTG GAT TAC GAA GTG CCA GAG TTT CAG AGT ATT. ACG
 Leu Asp Tyr Glu Val Pro Glu Phe Gln Ser Ile Thr
 1650 1660 1670 1680
 ATT CGG GTG GTA GCG ACC GAC AAC AAC GAC ACG
 Ile Arg Val Val Ala Thr Asp Asn Asn Asp Thr
 1690 1700 1710
 AGG CAC GTG GGC GTC GCG TTG GTT CAC ATT GAC CTC
 Arg His Val Gly Val Ala Leu Val His Ile Asp Leu
 1720 1730 1740 1750
 ATC AAT TGG AAC GAT GAG CAG CCG ATC TTC GAA CAC
 Ile Asn Trp Asn Asp Glu Gln Pro Ile Phe Glu His
 1760 1770 1780
 GCC GTG CAG ACC GTC ACC TTC GAC GAG ACT GAA GGC
 Ala Val Gln Thr Val Thr Phe Asp Glu Thr Glu Gly

FIG. 1D

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1790 1800 1810 1820
 GAG GGG TTC TTC GTC GCC AAG GCG GTT GCA CAC
 Glu Gly Phe Phe Val Ala Lys Ala Val Ala His
 1830 1840 1850
 GAC AGA GAC ATC GGG GAT GTC GTC GAG CAT ACT TTA
 Asp Arg Asp Ile Gly Asp Val Val Glu His Thr Leu
 1860 1870 1880 1890
 TTG GGT AAC GCT GTT AAC TTC CTG ACC ATC GAC
 Leu Gly Asn Ala Val Asn Phe Leu Thr Ile Asp
 1900 1910 1920
 AAA CTC ACC GGC GAC ATC CGC GTC TCA GCT AAC GAC
 Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp
 1930 1940 1950 1960
 TCC TTC AAC TAC CAT CGA GAA AGT GAA TTA TTT GTG
 Ser Phe Asn Tyr His Arg Glu Ser Glu Leu Phe Val
 1970 1980 1990
 CAG GTG CGA GCT ACA GAC ACG CTG GGC GAA CCC TTC
 Gln Val Arg Ala Thr Asp Thr Leu Gly Glu Pro Phe
 2000 2010 2020 2030
 CAC ACG GCG ACG TCA CAG CTG GTC ATA CGA CTA
 His Thr Ala Thr Ser Gln Leu Val Ile Arg Leu
 2040 2050 2060
 AAT GAC ATC AAC AAC ACG CCA CCC ACC TTA CGG CTG
 Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu
 2070 2080 2090 2100
 CCT CGA GGC AGT CCC CAA GTG GAG GAG AAC GTG
 Pro Arg Gly Ser Pro Gln Val Glu Glu Asn Val
 2110 2120 2130
 CCT GAT GGC CAC GTC ATC ACC CAG GAG TTA CGC GCC
 Pro Asp Gly His Val Ile Thr Gln Glu Leu Arg Ala
 2140 2150 2160 2170
 ACC GAC CCC GAC ACC ACG GCC GAT CTG CGC TTC GAG
 Thr Asp Pro Asp Thr Thr Ala Asp Leu Arg Phe Glu
 2180 2190 2200
 ATA AAC TGG GAC ACC TCT TTC GCC ACC AAG CAA GGC
 Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly

FIG. 1E

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2210 2220 2230 2240
 CGC CAG GCT AAC CCC GAC GAG TTT AGG AAT TGC
 Arg Gln Ala Asn Pro Asp Glu Phe Arg Asn Cys
 2250 2260 2270
 GTG GAA ATC GAG ACC ATC TTC CCC GAG ATT AAC AAC
 Val Glu Ile Glu Thr Ile Phe Pro Glu Ile Asn Asn
 2280 2290 2300 2310
 CGG GGA CTG GCT ATC GGC CGC GTT GTA GCG CGC
 Arg Gly Leu Ala Ile Gly Arg Val Val Ala Arg
 2320 2330 2340
 GAA ATC AGA CAC AAC GTG ACC ATA GAC TAC GAG GAG
 Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu
 2350 2360 2370 2380
 TTT GAG GTC CTC TCC CTC ACA GTG AGG GTG CGT GAC
 Phe Glu Val Leu Ser Leu Thr Val Arg Val Arg Asp
 2390 2400 2410
 CTT AAC ACC GTC TAC GGA GAC GAC TAC GAC GAA TCG
 Leu Asn Thr Val Tyr Gly Asp Asp Tyr Asp Glu Ser
 2420 2430 2440 2450
 ATG CTC ACA ATA ACT ATA ATC GAT ATG AAC GAC
 Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp
 2460 2470 2480
 AAC GCG CCG GTG TGG GTG GAG GGG ACT CTG GAG CAG
 Asn Ala Pro Val Trp Val Glu Gly Thr Leu Glu Gln
 2490 2500 2510 2520
 AAC TTC CGA GTC CGC GAG ATG TCG GCG GGC GGG
 Asn Phe Arg Val Arg Glu Met Ser Ala Gly Gly
 2530 2540 2550
 CTC GTG GTG GGC TCC GTG CGC GCG GAC GAC ATC GAC
 Leu Val Val Gly Ser Val Arg Ala Asp Asp Ile Asp
 2560 2570 2580 2590
 GGA CCG CTC TAC AAC CAA GTG CGA TAC ACC ATT TTC
 Gly Pro Leu Tyr Asn Gln Val Arg Tyr Thr Ile Phe
 2600 2610 2620
 CCT CGT GAA GAC ACA GAT AAG GAC CTG ATA ATG ATC
 Pro Arg Glu Asp Thr Asp Lys Asp Leu Ile Met Ile

FIG. 1F

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2630 2640 2650 2660
 GAC TTC CTC ACG GGT CAA ATT TCC GTG AAC ACA
 Asp Phe Leu Thr Gly Gln Ile Ser Val Asn Thr
 2670 2680 2690
 AGC GGC GCC ATC GAC GCG GAT ACT CCT CCA CGC TTC
 Ser Gly Ala Ile Asp Ala Asp Thr Pro Pro Arg Phe
 2700 2710 2720 2730
 CAC CTC TAC TAT ACA GTG GTC GCT AGT GAC CGA
 His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg
 2740 2750 2760
 TGC TCG ACA GAA GAT CCT GCA GAT TGC CCC CCT GAC
 Cys Ser Thr Glu Asp Pro Ala Asp Cys Pro Pro Asp
 2770 2780 2790 2800
 CCG ACT TAT TGG GAA ACC GAA GGA AAT ATC ACA ATC
 Pro Thr Tyr Trp Glu Thr Glu Gly Asn Ile Thr Ile
 2810 2820 2830
 CAC ATC ACC GAC ACG AAC AAC AAG GTC CCG CAG GCG
 His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala
 2840 2850 2860 2870
 GAA ACG ACT AAG TTC GAT ACC GTC GTG TAT ATT
 Glu Thr Thr Lys Phe Asp Thr Val Val Tyr Ile
 2880 2890 2900
 TAC GAG AAC GCA ACC CAC TTA GAC GAG GTG GTC ACT
 Tyr Glu Asn Ala Thr His Leu Asp Glu Val Val Thr
 2910 2920 2930 2940
 CTG ATA GCC AGT GAT CTT GAC AGA GAC GAA ATA
 Leu Ile Ala Ser Asp Leu Asp Arg Asp Glu Ile
 2950 2960 2970
 TAC CAC ACG GTG AGC TAC GTC ATC AAT TAT GCA GTG
 Tyr His Thr Val Ser Tyr Val Ile Asn Tyr Ala Val
 2980 2990 3000 3010
 AAC CCT CGA CTG ATG AAC TTC TTC TCC GTG AAC CGA
 Asn Pro Arg Leu Met Asn Phe Phe Ser Val Asn Arg
 3020 3030 3040
 GAG ACC GGC CTG GTG TAC GTG GAC TAT GAG ACC CAG
 Glu Thr Gly Leu Val Tyr Val Asp Tyr Glu Thr Gln

FIG. 1G

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3050 3060 3070 3080
 GGT AGT GGC GAG GTG CTG GAC CGT GAT GGT GAT
 Gly Ser Gly Glu Val Leu Asp Arg Asp Gly Asp
 3090 3100 3110
 GAA CCA ACG CAC CGT ATC TTC TTC AAC CTC ATC GAC
 Glu Pro Thr His Arg Ile Phe Phe Asn Leu Ile Asp
 3120 3130 3140 3150
 AAC TTC ATG GGG GAA GGA GAA GGT AAC AGA AAT
 Asn Phe Met Gly Glu Gly Glu Gly Asn Arg Asn
 3160 3170 3180
 CAG AAC GAC ACA GAA GTT CTC GTT ATC TTG TTG GAT
 Gln Asn Asp Thr Glu Val Leu Val Ile Leu Leu Asp
 3190 3200 3210 3220
 GTG AAT GAC AAT GCT CCT GAA TTG CCA CCG CCG AGC
 Val Asn Asp Asn Ala Pro Glu Leu Pro Pro Pro Ser
 3230 3240 3250
 GAA CTC TCT TGG ACT ATA TCT GAG AAC CTT AAG CAG
 Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln
 3260 3270 3280 3290
 GGC GTC CGT CTT GAA CCA CAT ATC TTC GCC CCG
 Gly Val Arg Leu Glu Pro His Ile Phe Ala Pro
 3300 3310 3320
 GAC CGC GAC GAG CCC GAC ACA GAC AAC TCC AGG GTC
 Asp Arg Asp Glu Pro Asp Thr Asp Asn Ser Arg Val
 3330 3340 3350 3360
 GGC TAC GAG ATC CTG AAC CTC AGC ACG GAG CGG
 Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg
 3370 3380 3390
 GAC ATC GAA GTG CCG GAG CTG TTT GTG ATG ATA CAG
 Asp Ile Glu Val Pro Glu Leu Phe Val Met Ile Gln
 3400 3410 3420 3430
 ATC GCG AAC GTC ACG GGA GAG CTG GAG ACC GCC ATG
 Ile Ala Asn Val Thr Gly Glu Leu Glu Thr Ala Met
 3440 3450 3460
 GAC CTC AAG GGA TAT TGG GGG ACG TAC GCT ATA CAT
 Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala Ile His

FIG. 1H

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3470 3480 3490 3500
ATA CGG GCA TTC GAC CAC GGC ATT CCG CAA ATG
Ile Arg Ala Phe Asp His Gly Ile Pro Gln Met
3510 3520 3530
TCC ATG AAC GAG ACA TAT GAG CTG ATC ATC CAT CCG
Ser Met Asn Glu Thr Tyr Glu Leu Ile Ile His Pro
3540 3550 3560 3570
TTC AAC TAC TAC GCG CCT GAG TTC GTC TTC CCG
Phe Asn Tyr Tyr Ala Pro Glu Phe Val Phe Pro
3580 3590 3600
ACC AAC GAT GCC GTC ATA CGA CTT GCG AGG GAA CGA
Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg
3610 3620 3630 3640
GCT GTA ATC AAT GGA GTT CTA GCG ACA GTG AAC GGA
Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly
3650 3660 3670
GAG TTC TTG GAG CGG ATA TCG GCG ACT GAT CCG GAC
Glu Phe Leu Glu Arg Ile Ser Ala Thr Asp Pro Asp
3680 3690 3700 3710
GGA CTC CAC GCG GGC GTC GTC ACC TTC CAA GTG
Gly Leu His Ala Gly Val Val Thr Phe Gln Val
3720 3730 3740
GTA GGC GAT GAG GAA TCA CAA CGG TAC TTT CAA GTA
Val Gly Asp Glu Glu Ser Gln Arg Tyr Phe Gln Val
3750 3760 3770 3780
GTT AAC GAT GGC GAG AAC CTC GGC TCG TTG AGG
Val Asn Asp Gly Glu Asn Leu Gly Ser Leu Arg
3790 3800 3810
TTA CTG CAA GCC GTT CCA GAG GAG ATC AGG GAG TTC
Leu Leu Gln Ala Val Pro Glu Glu Ile Arg Glu Phe
3820 3830 3840 3850
CGG ATA ACG ATT CGC GCT ACA GAC CAG GGA ACG GAC
Arg Ile Thr Ile Arg Ala Thr Asp Gln Gly Thr Asp
3860 3870 3880
CCA GGA CCG CTG TCC ACG GAC ATG ACG TTC AGA GTT
Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val

FIG. 11

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3890 3900 3910 3920
 GTT TTT GTG CCC ACG CAA GGA GAA CCT AGA TTC
 Val Phe Val Pro Thr Gln Gly Glu Pro Arg Phe
 3930 3940 3950
 GCG TCC TCA GAA CAT GCT GTC GCT TTC ATA GAA AAG
 Ala Ser Ser Glu His Ala Val Ala Phe Ile Glu Lys
 3960 3970 3980 3990
 AGT GCC GGC ATG GAA GAG TCT CAC CAA CTT CCT
 Ser Ala Gly Met Glu Glu Ser His Gln Leu Pro
 4000 4010 4020
 CTA GCA CAA GAC ATC AAG AAC CAT CTC TGT GAA GAC
 Leu Ala Gln Asp Ile Lys Asn His Leu Cys Glu Asp
 4030 4040 4050 4060
 GAC TGT CAC AGC ATT TAC TAT CGT ATT ATC GAT GGC
 Asp Cys His Ser Ile Tyr Tyr Arg Ile Ile Asp Gly
 4070 4080 4090
 AAC AGC GAA GGT CAT TTC GGC CTG GAT CCT GTT CGC
 Asn Ser Glu Gly His Phe Gly Leu Asp Pro Val Arg
 4100 4110 4120 4130
 AAC AGG TTG TTC CTG AAG AAA GAG CTG ATA AGG
 Asn Arg Leu Phe Leu Lys Lys Glu Leu Ile Arg
 4140 4150 4160
 GAA CAA AGT GCC TCC CAC ACT CTG CAA GTG GCG GCT
 Glu Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala
 4170 4180 4190 4200
 AGT AAC TCG CCC GAT GGT GGC ATT CCA CTT CCT
 Ser Asn Ser Pro Asp Gly Gly Ile Pro Leu Pro
 4210 4220 4230
 GCT TCC ATC CTT ACT GTC ACT GTT ACC GTG AGG GAG
 Ala Ser Ile Leu Thr Val Thr Val Thr Val Arg Glu
 4240 4250 4260 4270
 GCA GAC CCT CGT CCA GTG TTT GTG AGG GAA TTG TAC
 Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr
 4280 4290 4300
 ACC GCA GGG ATA TCC ACA GCG GAC TCC ATC GGC AGA
 Thr Ala Gly Ile Ser Thr Ala Asp Ser Ile Gly Arg

FIG. 1J

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4310 4320 4330 4340
 GAG CTG CTC AGA TTA CAT GCG ACC CAG TCT GAA
 Glu Leu Leu Arg Leu His Ala Thr Gln Ser Glu
 4350 4360 4370
 GGC TCG GCC ATT ACT TAT GCT ATA GAC TAC GAT ACA
 Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr Asp Thr
 4380 4390 4400 4410
 ATG GTA GTG GAC CCC AGC CTG GAG GCA GTG AGA
 Met Val Val Asp Pro Ser Leu Glu Ala Val Arg
 4420 4430 4440
 CAG TCG GCT TTC GTA CTG AAC GCT CAA ACC GGA GTG
 Gln Ser Ala Phe Val Leu Asn Ala Gln Thr Gly Val
 4450 4460 4470 4480
 CTG ACG CTT AAT ATC CAG CCC ACG GCC ACG ATG CAT
 Leu Thr Leu Asn Ile Gln Pro Thr Ala Thr Met His
 4490 4500 4510
 GGA CTG TTC AAA TTC GAA GTC ACA GCT ACT GAC ACG
 Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr
 4520 4530 4540 4550
 GCC GGC GCT CAG GAC CGC ACC GAC GTC ACC GTG
 Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val
 4560 4570 4580
 TAC GTG GTA TCC TCG CAG AAC CGC GTC TAC TTC GTG
 Tyr Val Val Ser Ser Gln Asn Arg Val Tyr Phe Val
 4590 4600 4610 4620
 TTC GTC AAC ACG CTG CAA CAG GTC GAA GAC AAC
 Phe Val Asn Thr Leu Gln Gln Val Glu Asp Asn
 4630 4640 4650
 AGA GAC TTT ATC GCG GAC ACC TTC AGC GCT GGG TTC
 Arg Asp Phe Ile Ala Asp Thr Phe Ser Ala Gly Phe
 4660 4670 4680 4690
 AAC ATG ACC TGC AAC ATC GAC CAA GTG GTG CCC GCT
 Asn Met Thr Cys Asn Ile Asp Gln Val Val Pro Ala
 4700 4710 4720
 AAC GAC CCC GTC ACC GGC GTG GCG CTG GAG CAC AGC
 Asn Asp Pro Val Thr Gly Val Ala Leu Glu His Ser

FIG. 1K

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4730 4740 4750 4760
 ACG CAG ATG CGC GGC CAC TTC ATA CGG GAC AAC
 Thr Gln Met Arg Gly His Phe Ile Arg Asp Asn
 4770 4780 4790
 GTA CCC GTA CTC GCT GAT GAG ATA GAA CAG ATC CGT
 Val Pro Val Leu Ala Asp Glu Ile Glu Gln Ile Arg
 4800 4810 4820 4830
 AGT GAC CTA GTC CTC CTG AGC TCG ATA CAA ACA
 Ser Asp Leu Val Leu Leu Ser Ser Ile Gln Thr
 4840 4850 4860
 ACG CTG GCG GCG CGA TCG CTG GTG TTG CAG GAC TTG
 Thr Leu Ala Ala Arg Ser Leu Val Leu Gln Asp Leu
 4870 4880 4890 4900
 TTG ACC AAC TCC AGC CCG GAC TCG GCG CCT GAC TCG
 Leu Thr Asn Ser Ser Pro Asp Ser Ala Pro Asp Ser
 4910 4920 4930
 AGC CTC ACG GTG TAC GTG CTG GCC TCA CTG TCT GCT
 Ser Leu Thr Val Try Val Leu Ala Ser Leu Ser Ala
 4940 4950 4960 4970
 GTG CTC GGT TTC ATG TGC CTT GTG CTA CTG CTT
 Val Leu Gly Phe Met Cys Leu Val Leu Leu Leu
 4980 4990 5000
 ACC TTC ATC ATC AGG ACT AGA GCG CTA AAC CGA CGG
 Thr Phe Ile Ile Arg Thr Arg Ala Leu Asn Arg Arg
 5010 5020 5030 5040
 TTG GAA GCC CTG TCG ATG ACG AAG TAC GGC TCA
 Leu Glu Ala Leu Ser Met Thr Lys Tyr Gly Ser
 5050 5060 5070
 CTG GAC TCT GGA TTG AAC CGC GCC GGC ATC GCC GCC
 Leu Asp Ser Gly Leu Asn Arg Ala Gly Ile Ala Ala
 5080 5090 5100 5110
 CCC GGC ACC AAC AAA CAC ACT GTG GAA GGC TCC AAC
 Pro Gly Thr Asn Lys His Thr Val Glu Gly Ser Asn
 5120 5130 5140
 CCT ATC TTC AAT GAA GCA ATA AAG ACG CCA GAT TTA
 Pro Ile Phe Asn Glu Ala Ile Lys Thr Pro Asp Leu

FIG. 1L

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5150 5160 5170 5180
GAT GCC ATT AGC GAG GGT TCC AAC GAC TCT GAT
Asp Ala Ile Ser Glu Gly Ser Asn Asp Ser Asp
5190 5200 5210
CTG ATC GGC ATC GAA GAT CTT CCG CAC TTT GGC AAC
Leu Ile Gly Ile Glu Asp Leu Pro His Phe Gly Asn
5220 5230 5240 5250
GTC TTC ATG GAT CCT GAG GTG AAC GAA AAG GCA
Val Phe Met Asp Pro Glu Val Asn Glu Lys Ala
5260 5270 5280
AAT GGT TAT CCC GAA GTC GCA AAC CAC AAC AAC AAC
Asn Gly Tyr Pro Glu Val Ala Asn His Asn Asn Asn
5290 5300 5310 5320
TTC GCT TTC AAC CCG ACT CCC TTC TCG CCT GAG TTC
Phe Ala Phe Asn Pro Thr Pro Phe Ser Pro Glu Phe
5330 5340 5350 5360
GTT AAC GGA CAG TTC AGA AAG ATC TAGAAGATAACAACA
Val Asn Gly Gln Phe Arg Lys Ile
5370 5380 5390 5400 5410
CTAGTTAAGATCATTAATTTTGGAGTTTGGGAATTAAGATTTTGGAAAG
5420 5430 5440 5450
GATAGTTGTGATAAGCCTGTGATTTTAAACTGTAATTGAAAAA
5460 5470 5480 5490 5500
AAAATTGAGACCTCCATTTAAGCTCTTGCTCTCATCTCATCAAATTTT
5510 5520 5530 5540 5550
ATAAAATGCCATTAGTCATTAAGATACTCGATTTAATTTAAGATTATT
5560 5570 5580
TAAGATATTATGTAAAATAAATATATTGTC

FIG. 1M

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SEQ ID NO. 2

Met Ala Val Asp Val Arg Ile Ala Ala Phe Leu Leu
 1 5 10
 Val Phe Ile Ala Pro Ala Val Leu Ala Gln Glu Arg
 15 20
 Cys Gly Tyr Met Thr Ala Ile Pro Arg Leu Pro Arg
 25 30 35
 Pro Asp Asn Leu Pro Val Leu Asn Phe Glu Gly Gln
 40 45
 Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala Pro Glu
 50 55 60
 Arg Asp Asp Leu Cys Met Asp Ala Tyr His Val Ile
 65 70
 Thr Ala Asn Leu Gly Thr Gln Val Ile Tyr Met Asp
 75 80
 Glu Glu Ile Glu Asp Glu Ile Thr Ile Ala Ile Leu
 85 90 95
 Asn Tyr Asn Gly Pro Ser Thr Pro Phe Ile Glu Leu
 100 105
 Pro Phe Leu Ser Gly Ser Tyr Asn Leu Leu Met Pro
 110 115 120
 Val Ile Arg Arg Val Asp Asn Gly Glu Trp His Leu
 125 130
 Ile Ile Thr Gln Arg Gln His Tyr Glu Leu Pro Gly
 135 140
 Met Gln Gln Tyr Met Phe Asn Val Arg Val Asp Gly
 145 150 155
 Gln Ser Leu Val Ala Gly Val Ser Leu Ala Ile Val
 160 165 CAD2
 Asn Ile Asp Asp Asn Ala Pro Ile Ile Gln Asn Phe
 170 175 180
 Glu Pro Cys Arg Val Pro Glu Leu Gly Glu Pro Gly
 185 190
 Leu Thr Glu Cys Thr Tyr Gln Val Ser Asp Ala Asp
 195 200
 Gly Arg Ile Ser Thr Glu Phe Met Thr Phr Arg Ile
 205 210 215

FIG. 2A

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Asp Ser Val Arg Gly Asp Glu Glu Thr Phe Tyr Ile
220 225
Glu Arg Thr Asn Ile Pro Asn Gln Trp Met Trp Leu
230 235 240
Asn Met Thr Ile Gly Val Asn Thr Ser Leu Asn Phe
245 250
Val Thr Ser Pro Leu His Ile Phe Ser Val Thr Ala
255 260
Leu Asp Ser Leu Pro Asn Thr His Thr Val Thr Met
265 270 275
Met Val Gln Val Ala Asn Val Asn Ser Arg Pro Pro
280 285

Arg Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu
290 295 300
Glu Lys Ser Tyr Gln Asn Phe Thr Val Arg Ala Ile
305 310
Asp Gly Asp Thr Glu Ile Asn Met Pro Ile Asn Tyr
315 320
Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser
325 330 335
Ile Glu Ala Leu Pro Gly Gly Lys Ser Gly Ala Val
340 345
Phe Leu Val Ser Pro Ile Asp Arg Asp Thr Leu Gln
350 355 360
Arg Glu Val Phe Pro Leu Thr Ile Val Ala Tyr Lys
365 370
Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val
375 380
Val Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro
385 390 395
Glu Pro Ile His Lys Glu Tyr Arg Leu Ala Ile Met
400 405
Glu Glu Thr Pro Leu Thr Leu Asn Phe Asp Lys Glu
410 415 420
Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala
425 430

FIG. 2B

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Gln	Tyr	Thr	Val	Arg	Leu	Glu	Ser	Val	Asp	Pro	Pro	
		435					440					
Gly	Ala	Ala	Glu	Ala	Phe	Tyr	Ile	Ala	Pro	Glu	Val	
445					450					455		
Gly	Tyr	Gln	Arg	Gln	Thr	Phe	Ile	Met	Gly	Thr	Leu	
			460					465				
Asn	His	Ser	Met	Leu	Asp	Tyr	Glu	Val	Pro	Glu	Phe	
	470					475					480	
Gln	Ser	Ile	Thr	Ile	Arg	Val	Val	Ala	Thr	Asp	Asn	
				485			CAD5			490		
Asn	Asp	Thr	Arg	His	Val	Gly	Val	Ala	Leu	Val	His	
		495					500					
Ile	Asp	Leu	Ile	Asn	Trp	Asn	Asp	Glu	Gln	Pro	Ile	
505					510					515		
Phe	Glu	His	Ala	Val	Gln	Thr	Val	Thr	Phe	Asp	Glu	
			520					525				
Thr	Glu	Gly	Glu	Gly	Phe	Phe	Val	Ala	Lys	Ala	Val	
	530					535					540	
Ala	His	Asp	Arg	Asp	Ile	Gly	Asp	Val	Val	Glu	His	
				545						550		
Thr	Leu	Leu	Gly	Asn	Ala	Val	Asn	Phe	Leu	Thr	Ile	
		555					560					
Asp	Lys	Leu	Thr	Gly	Asp	Ile	Arg	Val	Ser	Ala	Asn	
565					570					575		
Asp	Ser	Phe	Asn	Tyr	His	Arg	Glu	Ser	Glu	Leu	Phe	
			580					585				
Val	Gln	Val	Arg	Ala	Thr	Asp	Thr	Leu	Gly	Glu	Pro	
	590					595					600	
Phe	His	Thr	Ala	Thr	Ser	Gln	Leu	Val	Ile	Arg	Leu	
				605						610	CAD6	
Asn	Asp	Ile	Asn	Asn	Thr	Pro	Pro	Thr	Leu	Arg	Leu	
→		615					620					
Pro	Arg	Gly	Ser	Pro	Gln	Val	Glu	Glu	Asn	Val	Pro	
625					630					635		
Asp	Gly	His	Val	Ile	Thr	Gln	Glu	Leu	Arg	Ala	Thr	
			640					645				

FIG. 2C

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Asp	Pro	Asp	Thr	Thr	Ala	Asp	Leu	Arg	Phe	Glu	Ile	
	650					655					660	
Asn	Trp	Asp	Thr	Ser	Phe	Ala	Thr	Lys	Gln	Gly	Arg	
				665						670		
Gln	Ala	Asn	Pro	Asp	Glu	Phe	Arg	Asn	Cys	Val	Glu	
		675					680					
Ile	Glu	Thr	Ile	Phe	Pro	Glu	Ile	Asn	Asn	Arg	Gly	
685					690					695		
Leu	Ala	Ile	Gly	Arg	Val	Val	Ala	Arg	Glu	Ile	Arg	
			700					705				
His	Asn	Val	Thr	Ile	Asp	Tyr	Glu	Glu	Phe	Glu	Val	
	710				715						720	
Leu	Ser	Leu	Thr	Val	Arg	Val	Arg	Asp	Leu	Asn	Thr	
				725						730		
Val	Tyr	Gly	Asp	Asp	Tyr	Asp	Glu	Ser	Met	Leu	Thr	
		735					740					
Ile	Thr	Ile	Ile	Asp	Met	Asn	Asp	Asn	Ala	Pro	Val	
745					750					755	CAD7	
Trp	Val	Glu	Gly	Thr	Leu	Glu	Gln	Asn	Phe	Arg	Val	
→			760					765				
Arg	Glu	Met	Ser	Ala	Gly	Gly	Leu	Val	Val	Gly	Ser	
	770					775					780	
Val	Arg	Ala	Asp	Asp	Ile	Asp	Gly	Pro	Leu	Tyr	Asn	
				785					790			
Gln	Val	Arg	Tyr	Thr	Ile	Phe	Pro	Arg	Glu	Asp	Thr	
		795					800					
Asp	Lys	Asp	Leu	Ile	Met	Ile	Asp	Phe	Leu	Thr	Gly	
805					810					815		
Gln	Ile	Ser	Val	Asn	Thr	Ser	Gly	Ala	Ile	Asp	Ala	
			820					825				
Asp	Thr	Pro	Pro	Arg	Phe	His	Leu	Tyr	Tyr	Thr	Val	
	830					835					840	
Val	Ala	Ser	Asp	Arg	Cys	Ser	Thr	Glu	Asp	Pro	Ala	
				845					850			
Asp	Cys	Pro	Pro	Asp	Pro	Thr	Tyr	Trp	Glu	Thr	Glu	
		855					860					

FIG. 2D

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Gly	Asn	Ile	Thr	Ile	His	Ile	Thr	Asp	Thr	Asn	Asn
865					870					875	
					CAD8						
Lys	Val	Pro	Gln	Ala	Glu	Thr	Thr	Lys	Phe	Asp	Thr
			880					885			
Val	Val	Tyr	Ile	Tyr	Glu	Asn	Ala	Thr	His	Leu	Asp
890					895						900
Glu	Val	Val	Thr	Leu	Ile	Ala	Ser	Asp	Leu	Asp	Arg
			905						910		
Asp	Glu	Ile	Tyr	His	Thr	Val	Ser	Tyr	Val	Ile	Asn
	915						920				
Tyr	Ala	Val	Asn	Pro	Arg	Leu	Met	Asn	Phe	Phe	Ser
925					930					935	
Val	Asn	Arg	Glu	Thr	Gly	Leu	Val	Tyr	Val	Asp	Tyr
			940					945			
Glu	Thr	Gln	Gly	Ser	Gly	Glu	Val	Leu	Asp	Arg	Asp
950						955					960
Gly	Asp	Glu	Pro	Thr	His	Arg	Ile	Phe	Phe	Asn	Leu
				965					970		
Ile	Asp	Asn	Phe	Met	Gly	Glu	Gly	Glu	Gly	Asn	Arg
		975					980				
Asn	Gln	Asn	Asp	Thr	Glu	Val	Leu	Val	Ile	Leu	Leu
985					990					995	
								CAD9			
Asp	Val	Asn	Asp	Asn	Ala	Pro	Glu	Leu	Pro	Pro	Pro
			1000					1005			
Ser	Glu	Leu	Ser	Trp	Thr	Ile	Ser	Glu	Asn	Leu	Lys
1010						1015					1020
Gln	Gly	Val	Arg	Leu	Glu	Pro	His	Ile	Phe	Ala	Pro
				1025					1030		
Asp	Arg	Asp	Glu	Pro	Asp	Thr	Asp	Asn	Ser	Arg	Val
		1035					1040				
Gly	Tyr	Glu	Ile	Leu	Asn	Leu	Ser	Thr	Glu	Arg	Asp
1045					1050					1055	
Ile	Glu	Val	Pro	Glu	Leu	Phe	Val	Met	Ile	Gln	Ile
			1060					1065			
Ala	Asn	Val	Thr	Gly	Glu	Leu	Glu	Thr	Ala	Met	Asp
1070						1075					1080

FIG. 2E

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Leu	Lys	Gly	Tyr	Trp	Gly	Thr	Tyr	Ala	Ile	His	Ile	
				1085							1090	
Arg	Ala	Phe	Asp	His	Gly	Ile	Pro	Gln	Met	Ser	Met	
		1095					1100					
Asn	Glu	Thr	Tyr	Glu	Leu	Ile	Ile	His	Pro	Phe	Asn	
1105					1110	CAD10					1115	
Tyr	Tyr	Ala	Pro	Glu	Phe	Val	Phe	Pro	Thr	Asn	Asp	
			1120					1125				
Ala	Val	Ile	Arg	Leu	Ala	Arg	Glu	Arg	Ala	Val	Ile	
		1130				1135					1140	
Asn	Gly	Val	Leu	Ala	Thr	Val	Asn	Gly	Glu	Phe	Leu	
			1145						1150			
Glu	Arg	Ile	Ser	Ala	Thr	Asp	Pro	Asp	Gly	Leu	His	
		1155					1160					
Ala	Gly	Val	Val	Thr	Phe	Gln	Val	Val	Gly	Asp	Glu	
1165					1170					1175		
Glu	Ser	Gln	Arg	Tyr	Phe	Gln	Val	Val	Asn	Asp	Gly	
			1180					1185				
Glu	Asn	Leu	Gly	Ser	Leu	Arg	Leu	Leu	Gln	Ala	Val	
	1190					1195					1200	
Pro	Glu	Glu	Ile	Arg	Glu	Phe	Arg	Ile	Thr	Ile	Arg	
			1205						1210			
Ala	Thr	Asp	Gln	Gly	Thr	Asp	Pro	Gly	Pro	Leu	Ser	
		1215					1220					
Thr	Asp	Met	Thr	Phe	Arg	Val	Val	Phe	Val	Pro	Thr	
1225					1230	CAD11					1235	
Gln	Gly	Glu	Pro	Arg	Phe	Ala	Ser	Ser	Glu	His	Ala	
			1240					1245				
Val	Ala	Phe	Ile	Glu	Lys	Ser	Ala	Gly	Met	Glu	Glu	
	1250					1255					1260	
Ser	His	Gln	Leu	Pro	Leu	Ala	Gln	Asp	Ile	Lys	Asn	
			1265						1270			
His	Leu	Cys	Glu	Asp	Asp	Cys	His	Ser	Ile	Tyr	Tyr	
		1275				1280						
Arg	Ile	Ile	Asp	Gly	Asn	Ser	Glu	Gly	His	Phe	Gly	
1285					1290					1295		

FIG. 2F

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Leu	Asp	Pro	Val	Arg	Asn	Arg	Leu	Phe	Leu	Lys	Lys	
			1300					1305				
Glu	Leu	Ile	Arg	Glu	Gln	Ser	Ala	Ser	His	Thr	Leu	
	1310					1315					1320	
Gln	Val	Ala	Ala	Ser	Asn	Ser	Pro	Asp	Gly	Gly	Ile	
			1325						1330			
Pro	Leu	Pro	Ala	Ser	Ile	Leu	Thr	Val	Thr	Val	Thr	
	1335						1340					
Val	Arg	Glu	Ala	Asp	Pro	Arg	Pro	Val	Phe	Val	Arg	
1345					1350					1355		
Glu	Leu	Tyr	Thr	Ala	Gly	Ile	Ser	Thr	Ala	Asp	Ser	
			1360					1365				
Ile	Gly	Arg	Glu	Leu	Leu	Arg	Leu	His	Ala	Thr	Gln	
	1370					1375					1380	
Ser	Glu	Gly	Ser	Ala	Ile	Thr	Tyr	Ala	Ile	Asp	Tyr	
			1385						1390			
Asp	Thr	Met	Val	Val	Asp	Pro	Ser	Leu	Glu	Ala	Val	
	1395					1400						
Arg	Gln	Ser	Ala	Phe	Val	Leu	Asn	Ala	Gln	Thr	Gly	
1405					1410					1415		
Val	Leu	Thr	Leu	Asn	Ile	Gln	Pro	Thr	Ala	Thr	Met	
			1420					1425				
His	Gly	Leu	Phe	Lys	Phe	Glu	Val	Thr	Ala	Thr	Asp	
	1430					1435					1440	
Thr	Ala	Gly	Ala	Gln	Asp	Arg	Thr	Asp	Val	Thr	Val	
			1445						1450			
Tyr	Val	Val	Ser	Ser	Gln	Asn	Arg	Val	Tyr	Phe	Val	
	1455					1460						
Phe	Val	Asn	Thr	Leu	Gln	Gln	Val	Glu	Asp	Asn	Arg	
1465					1470					1475		
Asp	Phe	Ile	Ala	Asp	Thr	Phe	Ser	Ala	Gly	Phe	Asn	
			1480					1485				
Met	Thr	Cys	Asn	Ile	Asp	Gln	Val	Val	Pro	Ala	Asn	
	1490					1495					1500	
Asp	Pro	Val	Thr	Gly	Val	Ala	Leu	Glu	His	Ser	Thr	
			1505						1510			

FIG. 2G

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Gln	Met	Arg	Gly	His	Phe	Ile	Arg	Asp	Asn	Val	Pro	
			1515						1520			
Val	Leu	Ala	Asp	Glu	Ile	Glu	Gln	Ile	Arg	Ser	Asp	
1525					1530					1535		
Leu	Val	Leu	Leu	Ser	Ler	Ile	Gln	Thr	Thr	Leu	Ala	
			1540						1545			
Ala	Arg	Ser	Leu	Val	Leu	Gln	Asp	Leu	Leu	Thr	Asn	
	1550					1555					1560	
Ser	Ser	Pro	Asp	Ser	Ala	Pro	Asp	Ser	Ser	Leu	Thr	
			1565							1570		
Val	Thr	Val	Leu	Ala	Ser	Leu	Ser	Ala	Val	Leu	Gly	
		1575						1580				
Phe	Met	Cys	Leu	Val	Leu	Leu	Leu	Thr	Phe	Ile	Ile	
1585					1590					1595		
Arg	Thr	Arg	Ala	Leu	Asn	Arg	Arg	Leu	Glu	Ala	Leu	
			1600						1605			
Ser	Met	Thr	Lys	Tyr	Gly	Ser	Leu	Asp	Ser	Gly	Leu	
	1610					1615					1620	
Asn	Arg	Ala	Gly	Ile	Ala	Ala	Pro	Gly	Thr	Asn	Lys	
			1625							1630		
His	Thr	Val	Glu	Gly	Ser	Asn	Pro	Ile	Phe	Asn	Glu	
		1635						1640				
Ala	Ile	Lys	Thr	Pro	Asp	Leu	Asp	Ala	Ile	Ser	Glu	
1645					1650					1655		
Gly	Ser	Asn	Asp	Ser	Asp	Leu	Ile	Gly	Ile	Glu	Asp	
			1660						1665			
Leu	Pro	His	Phe	Gly	Asn	Val	Phe	Met	Asp	Pro	Glu	
	1670					1675					1680	
Val	Asn	Glu	Lys	Ala	Asn	Gly	Tyr	Pro	Glu	Val	Ala	
			1685							1690		
Asn	His	Asn	Asn	Asn	Phe	Ala	Phe	Asn	Pro	Thr	Pro	
		1695					1700					
Phe	Ser	Pro	Glu	Phe	Val	Asn	Gly	Gln	Phe	Arg	Lys	
1705					1710					1715		

Ile

FIG. 2H

mp EC1	EWVMPPIFVP	ENGK	GPFPORLNQL	KSNK	DRGKIFYY	ITGPGADSPPEGVFTIEKES
fat EC18	EDTVYSFDID	ENAGR	GYQVGQIV	ARDAD	LGONAQ	SYGVVSDWANDVFSNPO
pc42 EC2	ASPVITLAIP	ENTNI	GSLFPIPL	ASDRD	ANELQVAED	QEEKQQLIVM
HPT-1 EC1	IVTENIWKAPKV	EMVEN	STPHPIKITQ	VRWNP	DGAQYSLVD	KEKLPFPFSIDQE
BTRcad-1	ITANLGTQVLYMDE	EIEDE	ITAILNYNGPSTP	FIELP	ELSSYNLLMPVIRVDN	
BTRcad-2	QNFEPQVVP	ELGEP	GLTECTYQ	VSDAD	GRTSTEFMTFRIDSVR	
BTRcad-3	LEIFAVQQFE	EKSYQ	NFTVR	AIDGD	TEINMPINRYLITNEED	TFFSIEALPGGKS
BTRcad-4	IHKFYRLAIM	EETPL	TLNFDKEFG	FHKDK	LGONAQYTVRLESVD	PFGAAEFYIAPEV
BTRcad-5	EHAVQTVTFD	ETRGE	GFFVAKAV	AHARD	IGDVVEHTLLGNVNFLTIDKLT	
BTRcad-6	RLPRGSPQVE	ENVPD	AHVITQELR	AIDPD	ITADLRFEINWDTSFATK	QGRQANPDEFRCNCVEIETIP
BTRcad-7	VEGTLEQNFRVR	EMSAG	GLVVGSVR	ADDID	GPLYNQVRYTIFPRED	TDKDLIMIELPH
BTRcad-8	ETTKFDIVVYIY	ENATH	LDEVVTLI	ASDL	DRDEIYHMSVYINAVN	PRLMNFFSVNRET
BTRcad-9	PPPSSELSWTIS	ENLKO	GVRLEPHIF	APDR	DEPDTNSRVGYEILNLS	TERDIEVPEL FVMIQIIANVT
BTRcad-10	VFPTNDAVIRLAR	ERAVIN	GVLATVNGEFLERISA	IDPD	GLHAGVVT	FQVVGDEESQRYFQVVDND
BTRcad-11	ASSEHAVAFI	EKSA	GMEESHQPLPL	AGD	IKNHLCEDDCHSIYRI	IDGNSEGHF

Cadherin Consensus Motif ---E....---G.....---A.D.D.....

mp EC1	GWLLHMP	LDRE	KIVKELYGHAVSENGA	---	SVEEPMNISII	VTIDQNDNKPKE	(SEQ ID NO:8)
fat EC18	GMLTLTAR	LDYEE	VQHYILIVGAQDNGQP	---	SLSTITVYCNVLD	LDNDNAPIF	(SEQ ID NO:9)
pc42 EC2	GN	LDRE	RWDSYDLTIKVQDGGSP	---	PRATSALLRVT	VLIDNDNAPKE	(SEQ ID NO:10)
HPT-1 EC1	GDIYVTOP	IDREE	KDAYVFYAVAKDEYK	---	PLSYPLEI	THVKVKDIIDNPPITC	(SEQ ID NO:11)
BTRcad-1	GSASHH	HARQ	YELPGMQQYMFNVRVD	---	GQSLVAGVSLA	IVNIIDNAPIL	
BTRcad-2	GDEETFYIERTNIPNQWMLNMTIGVNTS	LNFT	SPLHIFSVTALDSL	---	PNTHVT	MMVQVANVNSRPPRW	
BTRcad-3	GAVFLV	IDRD	TLOREVFLTI VAYKYDEE	---	AFSTSTNV	VIIVTIDINDORPEP	
BTRcad-4	GYGRQTFIMGTLNHSM	IDYEV	PEFQSITIRVVA	TDNNDT	---	RHVGVALVHIDLINWDEQPIE	
BTRcad-5	GDIRVSANDSFN	YHRE	SELFVQVRATDILGQP	---	FHTATSQ	LVIRLNDIINNPITL	
BTRcad-6	-FPEININNRGLAIGRVVAREIRHNVT	IDYEE	FEVLSLTVRVRDLNTVYG	---	DDYDESM	LITITIDMNDNAPVM	
BTRcad-7	GSNFRE-HKRRIDANTPPRFHLYYTVA	SDRC	STEDPADCPPDP	---	YWETEG	NITITHITIDINKVPQA	
BTRcad-8	GLVYVDYETQSG	IDRD	GDEPTHRIFENLIDNFMGE	GE	GN	TEVLVILLVNDNAPEL	
BTRcad-9	GVEILNLS	TERDIEVPEL FVMIQIANVT	GELET	AMDLKGYWGTYA	YILAF	DHGIQMSMNETYELIHPFNYYAPEF	
BTRcad-10	GENLGSRLLLQAVPE	EIRE	FRITIRATDQGDTP	---	---	---	
BTRcad-11	GLDPVRNRLFLKKE	LI	RKDSASHTLQVAASNSPDGGI	---	---	PLPASILITVTVTREADPRVPE	

Cadherin Consensus Motif G.....---DRE.....---D.ND...P.F

FIG. 2I

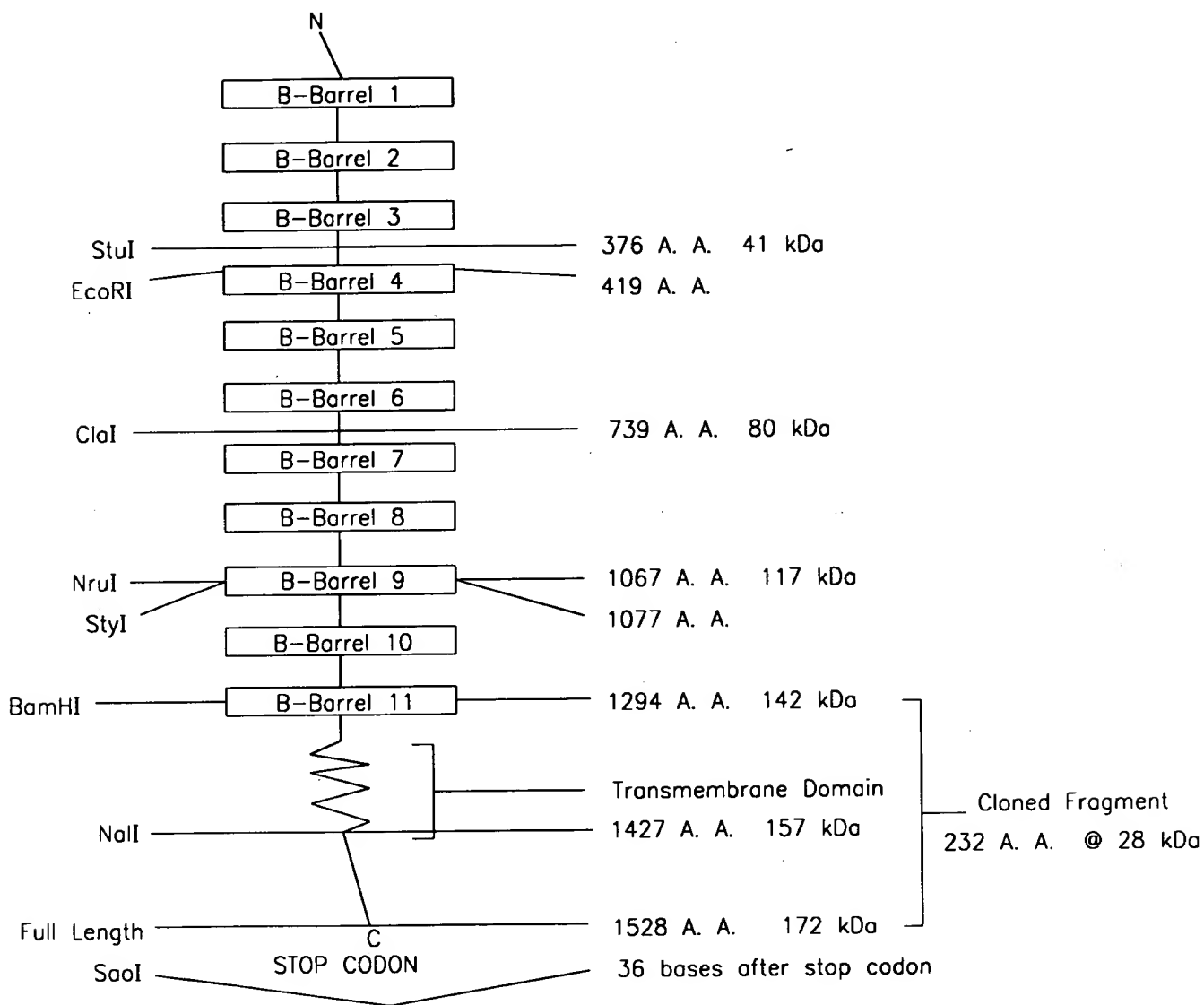


FIG. 3

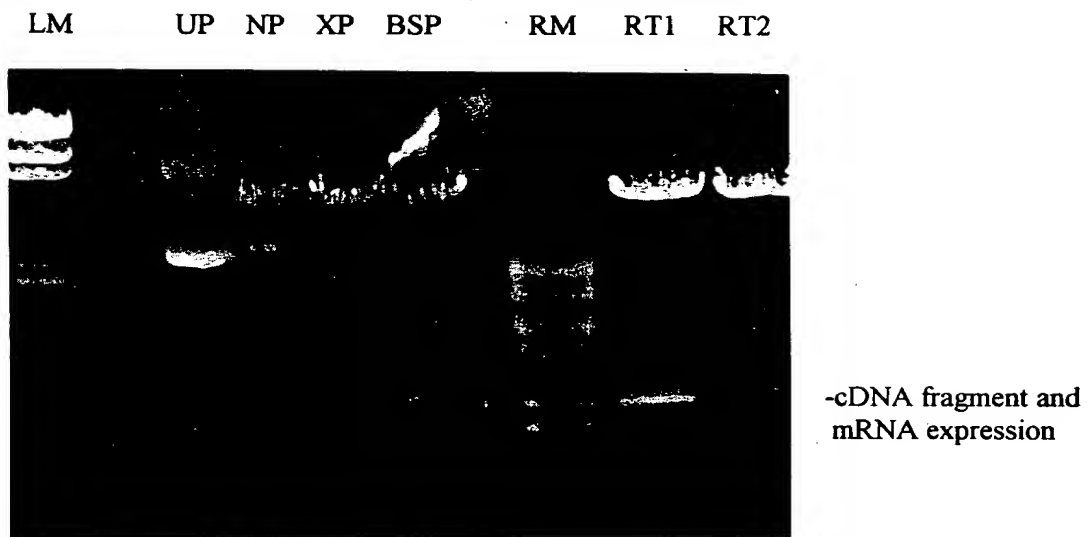


FIG. 4

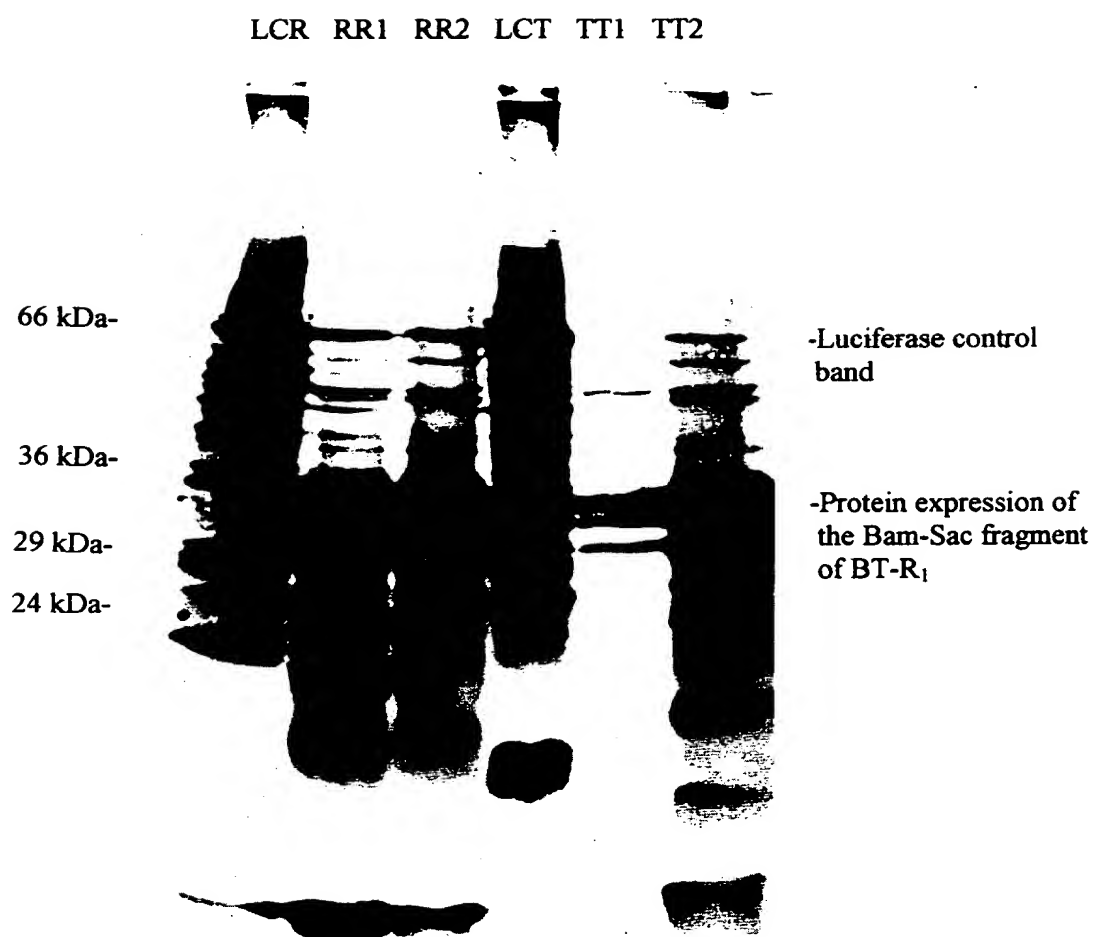


FIG. 5

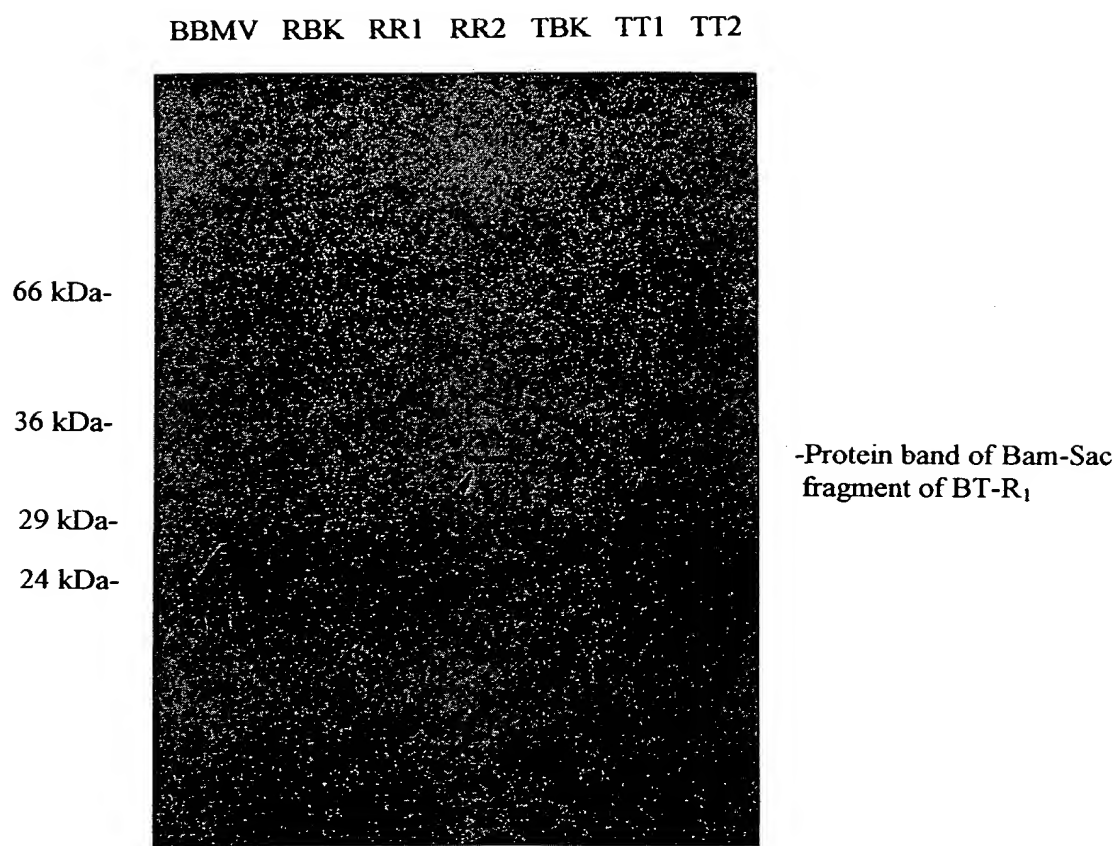


FIG. 6

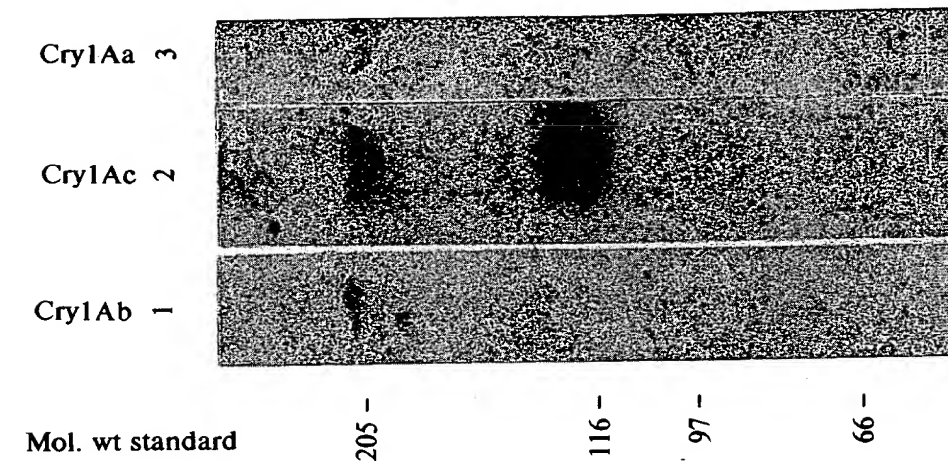


FIG. 7B

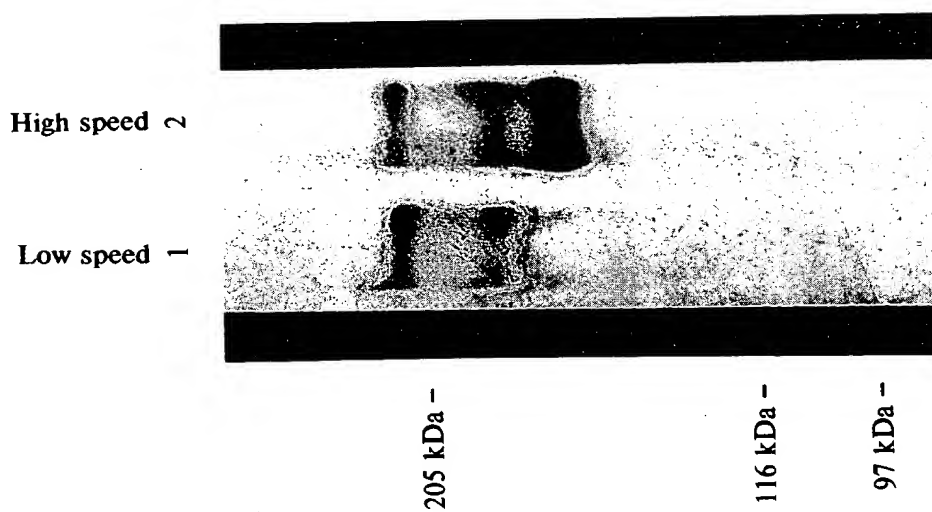


FIG. 7A

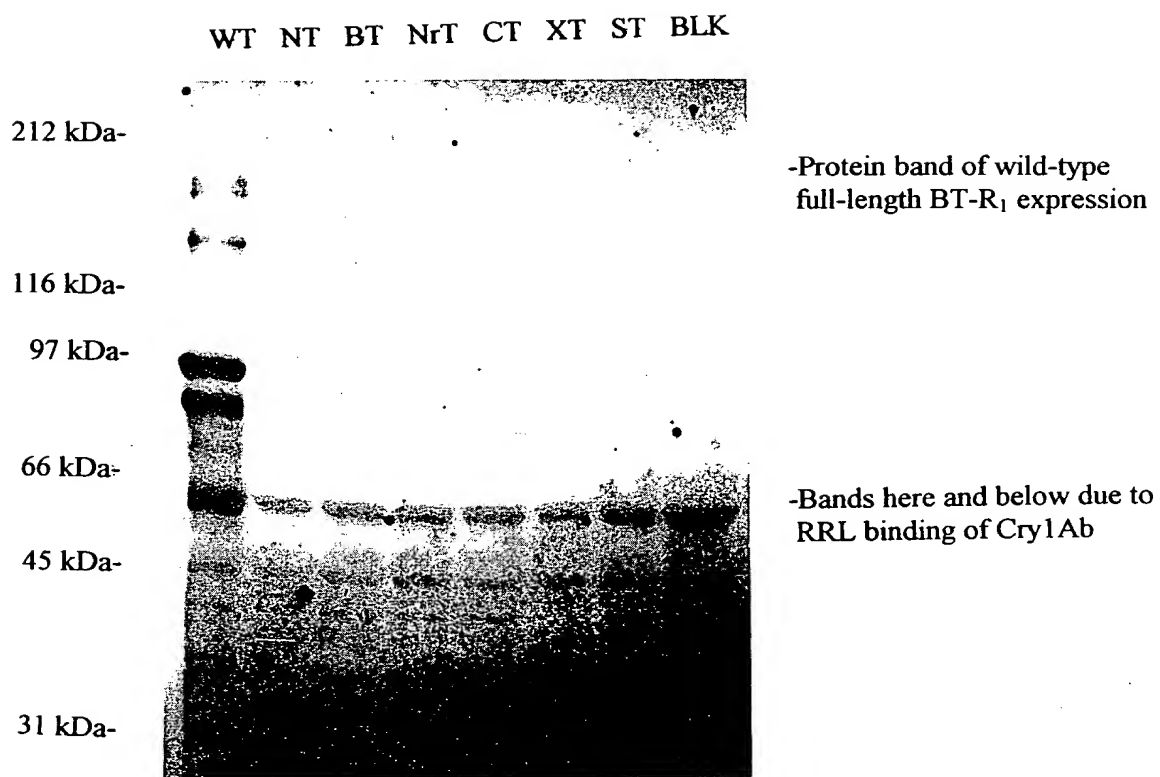


FIG. 8